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RAW SEQUENCE LISTING DATE: 02/12/2002 PATENT APPLICATION: US/09/813,271B TIME: 08:59:40

Input Set : N:\Crf3\02062002\I813271B.raw
Output Set: N:\CRF3\02122002\I813271B.raw

SEQUENCE LISTING

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3 (1) GENERAL INFORMATION:
             (i) APPLICANT: Nico Cerletti
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      5
            (ii) TITLE OF INVENTION: New process for the production of
      6
                                      biologically active protein
           (iii) NUMBER OF SEQUENCES: 13
      7
      8
            (iv) CORRESPONDENCE ADDRESS:
                  (A) ADDRESSEE: Novartis Patent Department
      9
     10
                  (B) STREET: 564 Morris Avenue
     11
                  (C) CITY: Summit
     12
                  (D) STATE: New Jersey
     13
                  (E) COUNTRY: USA
     14
                  (F) ZIP: 07901
             (V) COMPUTER READABLE FORM:
     15
     16
                  (A) MEDIUM TYPE: Floppy disk
     17
                  (B) COMPUTER: IBM PC compatible
                  (C) OPERATING SYSTEM: PC-DOS/MS-DOS
     18
                  (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
     19
            (vi) CURRENT APPLICATION DATA:
     20
C--> 21
                  (A) APPLICATION NUMBER: US/09/813,271B
C--> 22
                  (B) FILING DATE: 20-Mar-2001
     23
           (vii) PRIOR APPLICATION DATA:
     24
                  (A) APPLICATION NUMBER: PCT/EP95/02719
     25
                  (B) FILING DATE: 12-Jul-95
     26
                  (A) APPLICATION NUMBER: EPO 94810439.3
     27
                  (B) FILING DATE: 25-Jul-94
          (viii) ATTORNEY/AGENT INFORMATION:
     28
     29
                  (A) NAME: Pfeiffer, Hesna J. .
     30
                  (B) REGISTRATION NUMBER: 22640
                  (C) REFERENCE/DOCKET NUMBER: 4-20039C/C1C1/USN
     31
     32
            (ix) TELECOMMUNICATION INFORMATION:
                  (A) TELEPHONE: (908) 522-6940
     33
                  (B) TELEFAX: (908) 522-6955
     34
        (2) INFORMATION FOR SEQ ID NO: 1:
     35
             (i) SEQUENCE CHARACTERISTICS:
     36
     37
                  (A) LENGTH: 339 base pairs
     38
                  (B) TYPE: nucleic acid
     39
                  (C) STRANDEDNESS: double
                  (D) TOPOLOGY: linear
     40
            (ii) MOLECULE TYPE: cDNA to mRNA
     41
     42
           (iii) HYPOTHETICAL: NO
           (vii) IMMEDIATE SOURCE:
     43
                  (B) CLONE: E. coli LC137/pPLMu.hTGF-betal (DSM 5656)
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(ix) FEATURE:
45
             (A) NAME/KEY: CDS
46
47
             (B) LOCATION: 1..336
48
             (D) OTHER INFORMATION:/product= "human TGF-beta1"
49
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:
        GCC CTG GAC ACC AAC TAT TGC TTC AGC TCC ACG GAG AAG AAC TGC TGC
                                                                                  48
50
        Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
51
52
        GTG CGG CAG CTG TAC ATT GAC TTC CGC AAG GAC CTC GGC TGG AAG TGG
                                                                                  96
53
        Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
54
55
        ATC CAC GAG CCC AAG GGC TAC CAT GCC AAC TTC TGC CTC GGG CCC TGC
56
                                                                                 144
57
        Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
58
                 35
                                      40
                                                           45
        CCC TAC ATT TGG AGC CTG GAC ACG CAG TAC AGC AAG GTC CTG GCC CTG
                                                                                 192
59
        Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
60
                                                       60
61
             50
                                  55
                                                                                 240
        TAC AAC CAG CAT AAC CCG GGC GCC TCG GCG GCG CCG TGC TGC GTG CCG
62
        Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro
63
64
                              70
                                                   75
        CAG GCG CTG GAG CCG CTG CCC ATC GTG TAC TAC GTG GGC CGC AAG CCC
                                                                                 288
65
        Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
66
                          85
                                               90
67
        AAG GTG GAG CAG CTG TCC AAC ATG ATC GTG CGC TCC TGC AAG TGC AGC
                                                                                 336
68
        Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
69
70
                    100
                                         105
                                                                                 339
        TGA
71
   (2) INFORMATION FOR SEQ ID NO: 2:
73
        (i) SEQUENCE CHARACTERISTICS:
75
             (A) LENGTH: 112 amino acids
76
             (B) TYPE: amino acid
77
             (D) TOPOLOGY: linear
78
       (ii) MOLECULE TYPE: protein
79
       (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
        Ala Leu Asp Thr Asn Tyr Cys Phe Ser Ser Thr Glu Lys Asn Cys Cys
80
81
                           5
        Val Arg Gln Leu Tyr Ile Asp Phe Arg Lys Asp Leu Gly Trp Lys Trp
82
83
                                          25
84
        Ile His Glu Pro Lys Gly Tyr His Ala Asn Phe Cys Leu Gly Pro Cys
85
86
        Pro Tyr Ile Trp Ser Leu Asp Thr Gln Tyr Ser Lys Val Leu Ala Leu
87
                                  55
                                                       60
        Tyr Asn Gln His Asn Pro Gly Ala Ser Ala Ala Pro Cys Cys Val Pro
88
89.
        Gln Ala Leu Glu Pro Leu Pro Ile Val Tyr Tyr Val Gly Arg Lys Pro
90
91
                                               90
        Lys Val Glu Gln Leu Ser Asn Met Ile Val Arg Ser Cys Lys Cys Ser
92
93
                    100
                                         105
95 (2) INFORMATION FOR SEQ ID NO: 3:
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	96	(i) s	SEQUE	ENCE	CHAI	RACTI	ERIST	rics:	:										
	97		(A)	LENG	GTH:	339	base	e pai	irs										
	98		(B)	TYPI	Ξ: . nu	ıclei	ic ac	cid			•								
	99		(C)	STRA	ANDEI	ONESS	s: do	ouble	9										
	100		(D)	TOI	OLOG	3Y:]	Linea	ar											
	101	(ii)	MOL	ECULI	TYP	?E: 0	DNA	to r	nRNA										
	102	(vii)	IMME	EDIA	re so	OURCE	3:												
	103		(B)	CLO	ONE:	E. 0	coli	LC13	37/pI	PLMu	. hTGI	-bet	:a2 ((DSM	5657)			
	104	(ix)	FEAT	URE	:														
	105		(A)	NAI	ME/KE	ΞY: (CDS												
	106		(B)	LO	CATIO	ON:1.	336	5											
	107		(D)	OTI	HER]	INFO	RMAT	CON:	/prod	duct:	= "hı	ıman	TGF-	beta	a 2 "				
	108	(xi)	SEQU	JENCI	E DES	SCRIE	OITS	N: SI	EQ II	ON C	: 3:								
	109	GCT	TTG	GAT	GCG	GCC	TAT	TGC	TTT	AGA	AAT	GTG	CAG	GAT	AAT	TGC	TGC		48
	110	Ala	Leu	Asp	Ala	Ala	Tyr	Cys	Phe	Arg	Asn	Val	Gln	Asp	Asn	Cys	Cys		
w>				115			_		120					125					
	112	CTA	CGT	CCA	CTT	TAC	ATT	GAT	TTC	AAG	AGG	GAT	CTA	GGG	TGG	AAA	TGG	•	96
	113		Arg																
w>			130			-		135		_	-	-	140						
	115	ATA	CAC	GAA	CCC	AAA	GGG	TAC	AAT	GCC	AAC	TTC	TGT	GCT	GGA	GCA	TGC	1	44
	116		His																
W>		145				-	150	-				155	_				160		
	118	CCG	TAT	TTA	TGG	AGT	TCA	GAC	ACT	CAG	CAC	AGC	AGG	GTC	CTG	AGC	TTA	1	.92
	119		Tyr																
W>			- 4 -			165		-			170					175			
	121	тат	AAT	ACC	АТА		CCA	GAA	GCA	TCT		TCT	CCT	TGC	TGC	GTG	TCC	2	240
	122		Asn																
W>		-1-	11011		180	*				185				- 2 -	190				
" -	124	CAA	GAT	тта		CCT	СТА	ACC	ATT		TAC	TAC	ATT	GGC	AAA	ACA	CCC	2	288
	125		Asp																
W>				195	014				200		-1-	-1-		205	-1-				
" -	127		ATT		CAG	СТТ	тст	ААТ		АТТ	GTA	AAG	TCT		AAA	TGC	AGC	3	336
	128		Ile																
W>		215	210	014	0.2.11	Lou		215				-1-	220	-1-	-1-	-1-			
" ,	130	TAA																3	339
		(2) INFO		TON 1	FOR S	SEO '	א מז)· 4	•										
	133	• •	SEQ																
	134	(-)				: 112				9									,
	135		•	•		amino			201u.										
	136					GY:													
	137	(ii)																	
	138	(xi)				-	•		EO TI	סוא מ	٠ 4٠								
	139		Leu									Val	Gln	Asp	Asn	Cvs	Cvs		
	140	1		чэр	лти	<u>.</u> 5	- y -	Cys	1 110	9	10	, 41	0111	5		15	0,0		
	141		Arg	Dro	Leu	TTTT	Tle	Δen	Dho	Luc		Aan	Leu	G1 v	Trn		ጥተኮ		
	141	ьеи	vr. A	FIO	20	- Y -	116	rab	1 116	25	9	p	Lcu	- T J	30	_13			
	142	т1 ^	His	G111	-	T.376	<u> </u>	Фаль	Δen		Δan	Dho	Cve	בו∆		בוג	Cve		
	143	116	HIS	35	FIO	пуз	GTA	- J -	40	niu	11011	1116	Cys	45	CTY	1.1u	U ₁ U		
	145	Dro	Tyr		Пъъ	Ser	Ser	λen		Gln	Hic	Ser	Δνα		וים.Т	Ser	Len		
	140	PIO	TAT	⊔∈u	ттЪ	Set	261	rah	TIIT	GTII	TITO	ο ς τ	тту	vai	ьeu	Det	1104		

	146		50					55					60						
	147	Tyr	Asn	Thr	Ile	Asn		Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Ser		
	148	65					70					75					80		
	149	Gln	Asp	Leu	Glu	Pro	Leu	Thr	Ile	Leu	Tyr	Tyr	Ile	Gly	Lys	Thr	\mathtt{Pro}		
	150					85					90					95			
	151	Lys	Ile	Glu	Gln	Leu	Ser	Asn	Met	Ile	Val	Lys	Ser	Cys	Lys	Cys	Ser		
	152 ⁻				100					105					110				
	154	(2) INFO	RMAT:	ION I	FOR S	SEQ :	ID NO	D: 5	:										
	155	(i)	SEQU	JENCI	E CHA	ARAC	reri:	STIC	S:										
	156	•	(A)) LE	NGTH	: 339	9 bas	se pa	airs										
	157		(B)	TYI)	PE: 1	nucle	eic a	acid											
	158		(C)) STI	RANDI	EDNES	SS: 0	duot	le										
	159		(D)) TOI	POLO	GY: 3	linea	ar											
	160	(ii)	MOL	ECULI	E TYI	PE: 0	CDNA	to 1	mRNA										
	161	(vii)	IMMI	EDIA:	re so	OURC	Ξ:												
	162		(B)) CL	ONE:	E. 0	coli	LC1	37/p1	PLMu	. hTGI	r-bet	:a 3	(DSM	565	3)			
	163	(ix)	FEA:	TURE	:														
	164		(A)) NAI	ME/KI	EY: (CDS												
	165		(B)) LO	CATI	ON:1	336	5			•								
	166					INFO		-	_			ıman	TGF.	-beta	a3"				
	167	(xi)	SEQU	JENCI	E DES	SCRI	OITS	1: S	EQ II	ON C	: 5:								
	168		TTG																48
	169	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Arg	Asn	Leu	Glu	Glu	Asn	Cys	Cys		
M>				115					120					125					
	171		CGC																96
	172	Val	Arg	Pro	Leu	Tyr	Ile		Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	Trp		
M>			130					135					140						
	174		CAT															1	L 4 4
	175		His	Glu	Pro	Lys	_	Tyr	Tyr	Ala	Asn		Cys	Ser	Gly	Pro			
M>		145					150					155					160	_	
	177		TAC															1	L92
	178	Pro	Tyr	Leu	Arg		Ala	Asp	Thr	Thr		Ser	Thr	Val	Leu		Leu		
W>						165					170					175		_	
	180		AAC															2	240
	181	Tyr	Asn	Thr		Asn	Pro	Glu	Ala		Ala	Ser	Pro	Cys		Val	Pro		
W>					180					185					190			_	
	183		GAC															2	288
	184	GIn	Asp		GIu	Pro	Leu	Thr		Leu	Tyr	Tyr	vaı	_	Arg	Thr	Pro		
W>				195	a. a				200	ama	ama		m.c.m	205		mam	100	-	
	186		GTG															3	336
	187	Lys	Val	GIu	GIn	Leu	ser		мет	vaı	vaı	ьуs		Cys	·гАх	Cys	ser		
W>		ma1	210					215					220					-	20
	189	TGA				0 EC .	TD 17	٠. <i>د</i>	_									3	339
	191																		
	192	(1)	SEQU							_									
	193			•		: 112			aCld	S									
	194			•		amino													
	195	, 2 2 .	•	•		GY: :													
	196	(ii)	MOPI	PCOT)	L IXI	FE:]	orore	≈TU											

	(xi)	SEQU	JENCI	E DES	SCRII	OITS	N: SI	EQ II	ON C	: 6:							
198	Ala	Leu	Asp	Thr	Asn	Tyr	Cys	Phe	Arg	Asn	Leu	Glu	Glu	Asn	Cys	Cys	
199	1				5					10					15		
200	Val	Arg	Pro	Leu	Tyr	Ile	Asp	Phe	Arg	Gln	Asp	Leu	Gly	Trp	Lys	\mathtt{Trp}	
201				20					25					30			
202	Val	His	Glu	Pro	Lys	Gly	Tyr	Tyr	Ala	Asn	Phe	Cys	Ser	Gly	Pro	Cys	
203			35					40					45				
204	Pro	Tyr	Leu	Arg	Ser	Ala	Asp	Thr	Thr	His	Ser	Thr	Val	Leu	Gly	Leu	
205		50					55					60					
206	${ t Tyr}$	Asn	Thr	Leu	Asn	Pro	Glu	Ala	Ser	Ala	Ser	Pro	Cys	Cys	Val	Pro	
207	• 65					70					75					80	
208	Gln	Asp	Leu	Glu		Leu	Thr	Ile	Leu	_	Tyr	Val	Gly	Arg	Thr	Pro	
209					85					90					95		
210	Lys	Val	Glu		Leu	Ser	Asn	Met		Val	Lys	Ser	Cys	_	Cys	Ser	
211				100					105					110			
	(2) INFO																
214	(i)	SEQU															
215					: 336		_	airs									
216					nucle												
217					EDNES			Le									
218					GY:]												
219	(ii)										1				c		
220					OITS		iesc	= "3	recor	noina	ant 1	nybr:	וע גו	NA O	Γ		
221	(vii)						T (11)	27 /~1) T M	men.	- h a + :	-1/4	4 /4 E	\ h ~ + :	. 2		
222	(E. 0	3011	LCI.	2 / / Þ1	ьми	. IGF	-per	11 (4	4/45	ber	13		
223	(ix)																
224	• •				tiv. "	nn+ +	ont:	: do									
224	, ,	(A)	NAI	ME/KI	EY: r			ide									
225	, ,	(A)	NAI LO	ME/KI	ON:1	.132	2		inct:	= "N-	-tori	mi na	1 44	amiı	no		
225 226	acide of	(A) (B) (D)	NAI LOC OTI	ME/KI CATIO HER I	ON:1 INFOI	.132 RMAT	2		luct=	= "N	-teri	mina:	l 44	ami	no		
225 226 227	acids of	(A) (B) (D) huma	NAI LOC OTI	ME/KI CATIO HER I GF-bo	ON:1 INFOI	.132 RMAT	2		luct=	= "N·	-teri	minal	l 44	ami	no		
225 226 227 228	acids of	(A) (B) (D) huma	NAI LOC OTI IN TO	ME/KI CATIO HER I GF-bo	ON:1 INFOI eta1'	132 RMATI	2 [ON:,	/prod	luct=	= "N·	-teri	minal	l 44	ami	no		
225 226 227 228 229		(A) (B) (D) huma FEAC	NAI LOC OTI IN TO TURE NAI	ME/KI CATIO HER I GF-bo : ME/KI	ON:1 INFOI etal' EY: r	.132 RMATI	ON:,	/prod	luct=	= "N·	-teri	mina:	l 44	ami	no		
225 226 227 228 229 230		(A) (B) (D) huma FEAC (A)	NAI LOC OTI IN TO TURE NAI	ME/KICATION HER IN GF-box HE/KICATION	ON:1 INFOI etal' EY: r ON:13	132 RMATI nat_p	2 ION:, pept:	/prod									
225 226 227 228 229 230 231	(ix)	(A) (B) (D) huma FEAC (A) (B)	NAI LOC OTI IN TO FURE NAI LOC OTI	ME/KI CATIO HER I GF-be HE/KI CATIO HER I	ON:1 INFOI etal' EY: r ON:13	132 RMATI nat_p 333	2 ION:, pept:	/prod									
225 226 227 228 229 230 231 232	(ix)	(A) (B) huma FEAC (A) (B) huma) NAI) LOO) OTI TURE) NAI) LOO) OTI	ME/KI CATIO HER : GF-be : ME/KI CATIO HER : GF-be	ON:1 INFOI etal' EY: r ON:13	132 RMATI nat_p 333	2 ION:, pept:	/prod									
225 226 227 228 229 230 231 232 233	(ix)	(A) (B) huma FEAC (A) (B) (D) huma	NAI LOC TURE NAI LOC OTI	ME/KI CATIO HER : GF-be : ME/KI CATIO HER : GF-be :	ON:1 INFOI etal' EY: r ON:1: INFOI eta3'	132 RMATI nat_r nat_r RMATI	2 ION:, pept:	/prod								y.	
225 226 227 228 229 230 231 232 233 234	(ix)	(A) (B) (D) huma FEAC (B) (D) huma FEAC (A)) NAI) LOO) OTI TURE) NAI) LOO) OTI TURE TURE) NAI	ME/KI CATIC HER : GF-be : ME/KI CATIC HER : GF-be : ME/KI	ON:1 INFOI etal' EY: I ON:13 INFOI eta3'	132 RMATI nat_p 333 RMATI	ON:, pept:	/prod									
225 226 227 228 229 230 231 232 233	(ix)	(A) (B) (D) huma FEAC (A) (B) huma FEAC (A) (B)) NAI) LOO) OTI TURE) NAI) LOO) OTI TURE TURE) NAI) LOO) LOO	ME/KI CATIC HER : GF-be : ME/KI CATIC HER : GF-be : ME/KI CATIC	ON:1 INFOI etal' EY: r ON:13 INFOI eta3' EY: (132 RMATI nat_p 333 RMATI	OPEPT:	/prod	luct:	= "C·	-terr	minai	1 68	ami	no	<i>y</i> -	
225 226 227 228 229 230 231 232 233 234 235 236	(ix) acids of (ix)	(A) (B) huma FEAT (A) huma FEAT (A) (B) huma) NAI) LOO) OTI TURE) NAI) LOO TURE TURE) NAI TURE) NAI) LOO) OTI	ME/KI CATIC HER : GF-be : ME/KI CATIC HER : GF-be : ME/KI CATIC	ON:1 INFOI etal' EY: I ON:13 INFOI eta3'	132 RMATI nat_p 333 RMATI	OPEPT:	/prod	luct:	= "C·	-terr	minai	1 68	ami	no	,	
225 226 227 228 229 230 231 232 233 234 235 236	(ix)	(A) (B) (D) huma (A) (B) (D) huma FEAT (A) (B) (D)	NAI LOC TURE NAI LOC TURE NAI LOC NAI LOC NAI LOC NAI TURE NAI LOC NAI	ME/KI CATIO HER : GF-be CATIO HER : GF-be HE/KI CATIO HE/KI CATIO	ON:1 INFOI etal' EY: I ON:1 INFOI eta3' EY: (ON:1 INFOI	RMATI	pept: 336 ION:,	/prod ide /prod /prod	luct=	= "C:	-terr	minai	1 68	ami	no		
225 226 227 228 229 230 231 232 233 234 235 236 237	(ix) acids of (ix) TGF-beta: (xi)	(A) (B) (D) huma (A) (B) (D) huma FEAT (A) (B) (D)	NAI LOC TURE NAI LOC TURE NAI LOC TURE NAI LOC TURE NAI	ME/KI CATIO HER : GF-be CATIO HER : ME/KI CATIO HER : ME/KI CATIO HER : ME/KI CATIO HER :	ON:1 INFOI etal' EY: I ON:1 INFOI eta3' EY: (ON:1 INFOI	nat_r mat_r 333 RMATI	pept: 336 ION:, ION:, ION:,	/prod ide /prod /prod	luct=	= "C· = "hy : 7:	-tern	mina:	l 68 F-be	ami: ta na	no amed	TGC	48
225 226 227 228 229 230 231 232 233 234 235 236 237 238	(ix) acids of (ix) TGF-beta: (xi) GCC	(A) (B) huma FEAC (A) huma FEAC (A) (B) 1-3" SEQU	NAI LOC TURE NAI	ME/KICATION HER INTERPORT TO THE	ON:1 INFOI etal' EY: I ON:1 INFOI EY: (ON:1 INFOI SCRII	nat_r , , , , , , , , , , , , , , , , , , ,	pept: 336 ION:, ION:, TGC	/prod /prod /prod /prod EQ II	luct= luct= O NO AGC	= "C: = "hy : 7: TCC	-tern ybric ACG	nina: d TG	l 68 F-be	ami ta na	no amed TGC		48
225 226 227 228 229 230 231 232 233 234 235 236 237 238 239	(ix) acids of (ix) TGF-beta: (xi) GCC	(A) (B) (D) huma (A) (B) (D) huma FEAT (A) (B) (D) 1-3" SEQU CTG	NAI LOC TURE NAI	ME/KICATION HER INTERPORT TO THE	ON:1 INFOI etal' EY: I ON:1 INFOI EY: (ON:1 INFOI SCRII	nat_r , , , , , , , , , , , , , , , , , , ,	pept: 336 ION:, ION:, TGC	/prod /prod /prod /prod EQ II	luct= luct= O NO AGC	= "C: = "hy : 7: TCC	-tern ybric ACG	nina: d TG	l 68 F-be	ami ta na	no amed TGC		48
225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240	acids of (ix) TGF-beta: (xi) GCC Ala 1	(A) (B) (D) huma (A) (B) (D) huma FEAT (A) (B) (D) 1-3" SEQU CTG) NAI) LOC TURE) NAI) LOC COL TURE) ASP	ME/KI CATIO HER : GF-be CATIO HER : ME/KI CATIO HER : ACC Thr	ON:1 INFOI etal' EY: I ON:1 INFOI EY: (ON:1 INFOI AAC ASn	nat_past_side and side and sid	pept: 336 ION:, ION:, TGC	/prod /prod /prod TTC Phe	luct= NO AGC Ser	= "C = "hy : 7: TCC Ser 10	-terr ybrid ACG Thr	nina d TG GAG Glu	l 68 F-be AAG Lys	amin ta na AAC Asn	no TGC Cys 15	Cys	48 96
225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241	(ix) acids of (ix) TGF-beta (xi) GCC Ala 1 GTG	(A) (B) huma FEAT (A) (B) huma FEAT (A) (B) CTG Leu	NAI LOC OTI TURE NAI LOC OTI TURE NAI LOC OTI GAC ASP	ME/KICATION HER IN THE CATION HER IN THE CATION CATION HER IN THE	ON:1 INFOI EY: I ON:1 INFOI EY: (ON:1 INFOI SCRII AAC ASn 5	nat_past_state and state a	pept: 336 ION:, ION:, TGC Cys GAC	/prod /prod /prod TTC Phe	luct= O NO AGC Ser CGC	= "C' = "hy : 7: TCC Ser 10 AAG	ybric ACG Thr GAC	nina d TG GAG Glu CTC	l 68 F-bet AAG Lys GGC	amin ta na AAC Asn TGG	no TGC Cys 15 AAG	Cys TGG	
225 226 227 228 229 230 231 232 233 234 235 236 237 238 240 241 242 243 244	acids of (ix) TGF-beta (xi) GCC Ala 1 GTG Val	(A) (B) huma FEAT (A) (B) huma FEAT (A) (B) CTG CTG Leu CGG Arg	NAI LOC OTH TURE NAI LOC OTH TURE NAI LOC OTH GAC ASP	ME/KICATION HER IN SEPTION ME/KICATION ME/	ON:1 INFOI EY: I ON:1 INFOI EX: (ON:1 INFOI AAC ASn 5 TAC	RMATE RMATE RMATE RMATE RMATE CDS .336 RMATE TTY ATT Ile	Pept: 336 ION:, ION:, TGC Cys GAC Asp	/prod /prod /prod TTC Phe TTC	luct= O NO AGC Ser CGC Arg 25	= "C' = "hy : 7: TCC Ser 10 AAG Lys	ACG Thr GAC Asp	d TG GAG Glu CTC Leu	l 68 F-be [†] AAG Lys GGC Gly	amin AAC Asn TGG Trp 30	TGC Cys 15 AAG Lys	Cys TGG Trp	
225 226 227 228 229 230 231 232 233 234 235 236 237 238 240 241 242 243	acids of (ix) TGF-beta (xi) GCC Ala 1 GTG Val	(A) (B) huma FEAT (A) (B) huma FEAT (A) (B) CTG Leu CGG	NAI LOC OTI TURE NAI LOC NAI LOC NAI LOC OTI GAC ASP	ME/KI CATIO HER : GF-be CATIO HER : ME/KI CATIO HER : Thr CTG Leu 20 CCC	ON:1 INFOI EY: I ON:1 INFOI EX: (ON:1 INFOI AAC ASn TAC TYT AAG	MATE MATE MATE MATE CDS MATE CDS MATE TAT TYT ATT Ile GGC	2 ION:, Dept: 336 ION:, TON:, TGC Cys GAC Asp	/prod /prod /prod TTC Phe TTC Phe CAT	luct= NO AGC Ser CGC Arg 25 GCC	= "C' = "hy : 7: TCC Ser 10 AAG Lys	ACG Thr GAC Asp	d TG GAG Glu CTC Leu TGC	l 68 F-bet AAG Lys GGC Gly TCA	amin AAC Asn TGG Trp 30 GGC	TGC Cys 15 AAG Lys	Cys TGG Trp TGC	

VERIFICATION SUMMARY

DATE: 02/12/2002 TIME: 08:59:41 PATENT APPLICATION: US/09/813,271B

Input Set : N:\Crf3\02062002\1813271B.raw Output Set: N:\CRF3\02122002\I813271B.raw

L:21 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:] L:22 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:] L:111 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:114 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:117 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:120 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:123 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:126 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:129 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:3 L:170 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:173 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:176 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:179 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:182 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:185 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5 L:188 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:5